

RESULTS 7

ENTRY A43113 #type complete
Chemokine (C-C) receptor 5 - human
TITLE C-C CKR-5
ALTERNATE_NAMES #formal_name Homo sapiens #common_name man
ORGANISM #formal_name Homo sapiens #common_name man
DATE 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change
10-Sep-1997

ACCESSIONS A43113
REFERENCE A43113
*authors Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.

*journal Biochemistry (1996) 35:3362-3367
*title Molecular cloning and functional expression of a new human
GCC chemokine receptor gene.

SUMMARY #accession A43113
#status preliminary
#molecule_type mRNA
#residues 1-352 #label SAM
##cross-references GB:X9192; NID:91262810; PID:e199247; PID:91262811
#length 352 #molecular-weight 40524 #checksum 6685

Query Match Best Local Similarity 54.1%; Score 1496; DB 2; Length 352; Matches 182; Conservative 88; Mismatches 56; Indels 9; Gaps 9;

DB 20 COKINVQIAARLPLPVLSLVLIFGFVGVMVILLINGKRLSMTDIYLNLNLASIDF 79
OY 24 CIEKADTRALMAQVPPVPLSVTFGLIGVWVVMILKRRRLRINTNLYLNLAISDUF 83

DB 80 LIITVPPWAAHYAAQ-WDFGNTMCQLLTGLYXFIGFSGTGFILITIDRYLAVHWRALK 138
OY 84 LVTLPFWHIVRGHNWFGHGMCKLLSGPFYHTGLSEIFLILLTIDRYLAVHWAFLR 143

DB 139 ARVTFEGTVTSV-TWVVAFVAFASLPGIIFFRSOKQGHLHY-CSSHFPYSQ-YQFMKNFQQL 196
OY 144 ARTVGPVITSVTIVGVLAVLAALPEFIFYETE-ELFEEFLTCSALYPEDTVYS-WRHFHTL 201

DB 197 KIVILGLVLPLLVAVIC'USGILKTLRCNEKKHRRAVILIFTMIVYLFWADPVNIVL 256
OY 202 RMTIFCLVPLLMAICYGIGIKLRLCRS-KKIVKAIILFIVMAVFFWTVYINAIL 260

DB 257 LNTFOEF-FGLNINCSSNNRDOAMVYETLGTMTHCCINPIIAYFVGKFRNLYFEQKH 315
OY 261 LKSYOSILFG-NDCCERTKHLDDLVMLVTEVIAVSHCCMNPIVAFVGERRKYLRHFFHRH 319

DB 315 IAKRFFCCKCSIFQEAPEERASVVTSTFQEISV 350
OY 320 ILMHLGRYVPPFLPSEKLETRSSV-SPSTAEPELSI 353

RESULTS 8

ENTRY S55594 #type complete
G protein-coupled receptor 81 - equine herpesvirus 2
TITLE #formal_name equine herpesvirus 2
DATE 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change
09-Sep-1997

ACCESSIONS S55594
REFERENCE S55594
*authors Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.

*journal J. Mol. Biol. (1995) 249:520-528
*title The DNA sequence of equine herpesvirus 2.

*accession S55594
#status preliminary; nucleic acid sequence not shown
#molecule_type DNA
#residues 1-383 #label TEL
##cross-references GB:020824; NID:9695172; PID:9559173
KEYWORDS G protein-coupled receptor
SUMMARY #length 383 #molecular-weight 43667 #checksum 1663

RESULTS 9

SEQUENCE COMPARISON A

RESULTS 9

ENTRY JC2443 #type complete
TITLE Chemokine (C-C) receptor 2, splice form B - human
ALTERNATE_NAMES C-C CKR-2; monocyte chemoattractant protein 1 receptor;
#formal_name Homo sapiens #common_name man
ORGANISM Monocyte chemoattractant protein 1 receptor
DATE 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change
10-Sep-1997

ACCESSIONS JC2443; 138463
REFERENCE JC2443
*authors Yamagami, S.; Tokuda, Y.; Ishii, K.; Tanaka, H.; Endo, N.; Bloch, M.

*journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
*title Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

*accession JC2443
#molecule_type mRNA
#residues 1-360 #label YAM
##cross-references DDBJ:D29984; NID:9531246; PID:d1006817; PID:9531247

REFERENCE A53477
*authors Chao, I.F.; Myers, S.J.; Herman, A.; Franci, C.; Connolly, A.J.; Coughlin, S.R.

*journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:2752-2756
*title Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternate splicing of the carboxyl-terminal tails.

*accession 138463
#status Preliminary
#molecule_type mRNA
#residues 1-360 #label RES
##cross-references MUID:94195821

GENETICS
*gene GDB:CMKBR2
#cross-references GDB:337364; OMIM:601267
#map_position 3p21-3p21

KEYWORDS alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein

FEATURES
43-70
81-100
115-136
155-178
207-226
244-268

#domain transmembrane #status predicted #label TM1
#domain transmembrane #status predicted #label TM2
#domain transmembrane #status predicted #label TM3
#domain transmembrane #status predicted #label TM4
#domain transmembrane #status predicted #label TM5
#domain transmembrane #status predicted #label TM6

287-309
14

SUMMARY *length 360 #molecular-weight 41063 #checksum 1732

Query Match 52.0%; Score 1438; DB 2; Length 360;
Best Local Similarity 53.4%; Pred. No. 5.17e-187;
Matches 183; Conservative 87; Mismatches 63; Indels 10; Gaps 8;

Db 21 TTFDDYDYGAPCHKFDVKGQIAQQLPPLYSVLFEGVGNMLVLLINCKKLUCLDIY 80
Oy 14 TSYD-DVGLCERADTRALMAOFVPLVPLVFTFGLLGNVVVMLIKYRRLRINTNLY 72

Db 81 LNLNAISDLEFLITPLWAHSA ANEWVFGNAMCKLFTGLYHIGFGIFILLTDY 139
Oy 73 LNLNAISDLEFLVLPFWHVVHVRGHNWFGHGMCKLSSGFTGLYHIGFGIFILLTDY 132

Db 140 LALVHAFALKARTVTFGVVTSVTLVAVAFASVPGIIFTKCQKEDSVVCGPYF-R- 196
Oy 133 LALVHAFALKARTVTFGVVTSVTLVAVAFASVPGIIFTKCQKEDSVVCGPYF-R- 192

Db 197 -GWNNEHTIMRNIGLVLPLIMIVCGIQLKLTLCRKEKKRRAVRYFTIMIVPLF 255
Oy 193 YSWRFHTLMTFCLVPLVMAICYTGIIKTLRCPS-KKKYKAIRLIFVMAVFF 251

Db 256 WTPYNNIVLNTFOQEF-FGLSNCESTSQDQATOVTETLGMTHCINPFIYAFGEKRR 314
Oy 252 WTPYNNIVLNTFOQEF-FGLSNCESTSQDQATOVTETLGMTHCINPFIYAFGEKRR 310

Db 315 YLSVFRKHTKFRCKQCPFYRETVDGVVSTNTSTGEFVS 357
Oy 311 YLRHFFPHBLMLHGLRYIPFLPSEKLE-RQSSVSPSTAELS 352

RESULT 10

ENTRY 149340 #type complete
TITLE MIP-1 alpha receptor like-1 - mouse
ORGANISM #formal_name Mus musculus #common_name house mouse
DATE 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change
28-Feb-1997

ACCESSIONS 149340
REFERENCE Gao, J. L.; Murphy, P. M.
authors J. Biol. Chem. (1995) 270:17494-17501
#Journal Cloning and differential tissue-specific expression of three
#title mouse beta chemokine receptor-like genes, including the
gene for a functional macrophage inflammatory protein-1
alpha receptor.
#cross-references MURD:95340546

#accession 149340
#status preliminary
#molecule_type mRNA
#residues 1-374 #label RES
#cross-references EMBL:003882; NID:9472555; PID:9472556

GENETICS
#gene GDB:CMBR2
#cross-references GDB:337364; OMIM:601267
#map_position 3p21-3p21

KEYWORDS alternative splicing; G protein-coupled receptor;
glycoprotein; transmembrane protein

FEATURE 44-58
#domain transmembrane #status predicted #label TM1
79-99 #domain transmembrane #status predicted #label TM2
115-136 #domain transmembrane #status predicted #label TM3
150-178 #domain transmembrane #status predicted #label TM4
200-226 #domain transmembrane #status predicted #label TM5
244-265 #domain transmembrane #status predicted #label TM6
292-309 #domain transmembrane #status predicted #label TM7
14 #predicted
#disulfide_bonds #status predicted

SUMMARY 32-277, 113-190 #length 374 #molecular-weight 41914 #checksum 5414
Query Match 48.9%; Score 1352; DB 2; Length 374;
Best Local Similarity 56.2%; Pred. No. 3.51e-174;
Matches 168; Conservative 50; Mismatches 50; Indels 9; Gaps 7;

Query Match 51.8%; Score 1433; DB 2; Length 356;
Best Local Similarity 52.0%; Pred. No. 2.88e-186; Length 356;
Matches 173; Conservative 78; Mismatches 80; Indels 2; Gaps 2;

Db 22 GFLCFSINRAGFTVPTPLYSVLFVIGVHVLVVLQHKLRLRNTSTVLFNLAISD 81
Oy 21 GLICEKADKRALMAOFVPLVPLSFLVFTGGLGIVNVVWMLIKYRRLRINTNLYLNLAISD 80

Db 21 TTFDDYDYGAPCHKFDVKGQIAQQLPPLYSVLFEGVGNMLVLLINCKKLUCLDIY 80
Oy 14 TSYD-DVGLCERADTRALMAOFVPLVPLVFTFGLLGNVVVMLIKYRRLRINTNLY 72

Db 81 LNLNAISDLEFLITPLWAHSA ANEWVFGNAMCKLFTGLYHIGFGIFILLTDY 139
Oy 73 LNLNAISDLEFLVLPFWHVVHVRGHNWFGHGMCKLSSGFTGLYHIGFGIFILLTDY 132

Db 82 LVFUSTLPLFADYIMKGDNIFGNGNACKEVSGFVYGLYSDMFFITLTDYLAHVHF 141
Oy 81 LLFLVLTPLFVHIVYVRGHNWFGHGMCKLSSGFTGLYSEIFFILLTDYLAHVHF 140

Db 142 ALRARTVTFGIISSITWVLAVALSIPCLCYVF-KSOMETYHCRALRKRKSLRFQ 200
Oy 141 ALRARTVTFGIVTSIVWGLAVLAALP-PRIFYTEELFEETLCSALYPEDTVSWRHF 199